

L Number	Hits	Search Text	DB	Time stamp
1	6	vogeli-gabriel.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
2	20	lind-peter.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
3	12	parodi-luis-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
4	3	wood-linda-s.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
5	2	hiebsch-ronald-r.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
6	3085	g adj protein adj coupled adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:31
7	1174	(g adj protein adj coupled adj receptor) same human	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:32

## 09714449 Results

SEQ ID NO: 85

## SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
	1	1020	100.0	1020	6	AX147840	AX147840 Sequence
	2	980.8	96.2	1081	6	AX458238	AX458238 Sequence
	3	980.8	96.2	1092	9	AF370886	AF370886 Homo sapi
	4	980.8	96.2	1414	9	AB065877	AB065877 Homo sapi
	5	980.8	96.2	9905	6	AX379470	AX379470 Sequence
c	6	980.8	96.2	67645	9	AL356486	AL356486 Human DNA
	7	980.8	96.2	156555	9	AC026756	AC026756 Homo sapi
	8	979.2	96.0	1729	6	AX191332	AX191332 Sequence
	9	977.8	95.9	1014	6	AX148186	AX148186 Sequence
	10	977.8	95.9	1014	6	AX379468	AX379468 Sequence
	11	977.8	95.9	1014	6	AX384211	AX384211 Sequence
	12	977.8	95.9	1014	9	AB083598	AB083598 Homo sapi
	13	977.8	95.9	1014	9	AF411109	AF411109 Homo sapi
	14	976.2	95.7	1014	6	AX305130	AX305130 Sequence
	15	976.2	95.7	1014	6	AX464561	AX464561 Sequence
c	16	701.4	68.8	202838	2	AC108794	AC108794 Mus muscu
c	17	578	56.7	578	6	AX147814	AX147814 Sequence
	18	335	32.8	2245	6	AX384210	AX384210 Sequence

## SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
	1	1020	100.0	1020	22	AAH51011	Human nGPCR54 codi
	2	980.8	96.2	1288	24	ABL56197	Human P2Y1-li enco
	3	980.8	96.2	5435	24	ABL56198	Human P2Y1-li enco
	4	980.8	96.2	9905	24	AAK98324	Human purinergic-r
	5	979.2	96.0	1729	22	AAS08362	Human cDNA encodin
	6	979.2	96.0	1729	23	ABV24026	Human prostate exp
	7	979.2	96.0	1729	23	ABV25767	Human prostate exp
	8	979.2	96.0	1729	23	ABV29909	Human prostate exp
	9	979.2	96.0	1729	23	ABV30024	Human prostate exp
	10	977.8	95.9	1014	22	AAS07948	Human cDNA encodin
	11	977.8	95.9	1014	24	ABN85630	Human P2Y-like rec
	12	977.8	95.9	1014	24	ABK11381	Human DNA encoding
	13	977.8	95.9	1014	24	AAK98323	Human purinergic-r
	14	976.2	95.7	1014	24	ABQ78847	Human G-protein co
	15	976.2	95.7	1014	24	AAD34278	Human AXOR89 (G-pr
	16	976.2	95.7	1014	24	AAD26370	Human G-protein co
	17	974.8	95.6	1011	24	AAL43942	Human G protein-co
	18	794.8	77.9	831	24	ABN85629	Human P2Y-like rec
	19	726.2	71.2	1313	22	AAK52430	Human polynucleoti
c	20	578	56.7	578	22	AAH50998	Human nGPCR54 codi
c	21	562.8	55.2	740	23	ABV15662	Human prostate exp
c	22	476.6	46.7	545	22	ABA08326	Human P2Y purinoce
c	23	476.6	46.7	545	22	AAK53414	Human polynucleoti
c	24	426.2	41.8	539	23	ABV39127	Human prostate exp

## RESULT 1

AAH51011

ID AAH51011 standard; DNA; 1020 BP.

XX

AC AAH51011;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR54 coding sequence #2.

XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;

KW signal transduction; schizophrenia; thyroid disorder; renal failure;  
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;  
KW cardiovascular disease; proliferative disorder; hormonal disorder;  
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;  
KW attention deficit-hyperactivity disorder/attention deficit disorder;  
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;  
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;  
KW neuroprotective; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200136473-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000WO-US31581.  
XX  
PR 16-NOV-1999; 99US-0165838.  
PR 17-NOV-1999; 99US-0166071.  
PR 19-NOV-1999; 99US-0166678.  
PR 28-DEC-1999; 99US-0173396.  
PR 22-FEB-2000; 2000US-0184129.  
PR 28-FEB-2000; 2000US-0185421.  
PR 28-FEB-2000; 2000US-0185554.  
PR 02-MAR-2000; 2000US-0186530.  
PR 03-MAR-2000; 2000US-0186811.  
PR 09-MAR-2000; 2000US-0188114.  
PR 17-MAR-2000; 2000US-0190310.  
PR 21-MAR-2000; 2000US-0190800.  
PR 20-APR-2000; 2000US-0198568.  
PR 02-MAY-2000; 2000US-0201190.  
PR 08-MAY-2000; 2000US-0203111.  
PR 25-MAY-2000; 2000US-0207094.  
XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;  
PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;  
XX  
DR WPI; 2001-389826/41.  
DR P-PSDB; AAG80971.  
XX  
PT New G protein-coupled receptor (nGPCR-x) and its encoding  
PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -  
XX  
PS Claim 4; Page 91; 261pp; English.  
XX  
CC The present invention relates to novel G protein-coupled receptors  
CC (nGPCR<sub>x</sub>; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,  
CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present  
CC sequence is the coding sequence for one such G protein-coupled receptor.  
CC GPCRs are also known as seven transmembrane receptors and function in  
CC signal transduction. The nGPCR<sub>x</sub> coding sequences are useful for  
CC screening a human to diagnose a disorder affecting the brain or a genetic  
CC predisposition, specifically schizophrenia. nGPCR<sub>x</sub> are useful for  
CC identifying compounds useful for treating schizophrenia. Detection of  
CC nGPCR<sub>x</sub> in a sample is useful as a diagnostic tool for diseases or  
CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,  
CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular  
CC diseases, proliferative disorders and hormonal disorders. Modulators of  
CC nGPCR<sub>x</sub> activity have the utility for treating neurological disorders,  
CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity  
CC disorder/attention deficit disorder), and neuronal disorders such as  
CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.  
CC Additional disorders include inflammatory conditions (e.g. Crohn's  
CC disease), rheumatoid arthritis, autoimmune disorders, cancers,  
CC respiratory ailments such as asthma, and inflammatory diseases e.g.  
CC inflammatory bowel disease.  
XX  
SQ Sequence 1020 BP; 261 A; 263 C; 190 G; 306 T; 0 other;

Query Match 100.0%; Score 1020; DB 22; Length 1020;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-287;  
 Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ACCATGAATGAGCCACTAGACTATTAGCAAATGCTTCTGATTTCGGATTATGCAGCT	60
Db	1 ACCATGAATGAGCCACTAGACTATTAGCAAATGCTTCTGATTTCGGATTATGCAGCT	60
Qy	61 GCTTTTGGAAATTGCACTGATGAAAACATCCCACCAAGATGCACTACCTCCCTGTTATT	120
Db	61 GCTTTTGGAAATTGCACTGATGAAAACATCCCACCAAGATGCACTACCTCCCTGTTATT	120
Qy	121 TATGGCATTATCTTCCTCGTGGGATTTCAGGCAATGCAGTAGTGTATCCACTTACATT	180
Db	121 TATGGCATTATCTTCCTCGTGGGATTTCAGGCAATGCAGTAGTGTATCCACTTACATT	180
Qy	181 TTCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTATGCTGAACCTGGCTGCACAGAT	240
Db	181 TTCAAAATGAGACCTTGGAAAGAGCAGCACCATCATTATGCTGAACCTGGCTGCACAGAT	240
Qy	241 CTGCTGTATCTGACCAGCCTCCCCCTCCTGATTCACTACTATGCCAGTGGCGAAACTGG	300
Db	241 CTGCTGTATCTGACCAGCCTCCCCCTCCTGATTCACTACTATGCCAGTGGCGAAACTGG	300
Qy	301 ATCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCATTCAACCTGTATAGC	360
Db	301 ATCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCATTCAACCTGTATAGC	360
Qy	361 AGCATCCCTTCCACCTGTGTTCAGCATCTCCGCTACTGTGTGATCATTACCCAATG	420
Db	361 AGCATCCCTTCCACCTGTGTTCAGCATCTCCGCTACTGTGTGATCATTACCCAATG	420
Qy	421 AGCTGCTTTCCATTCAACAAACTCGATGTGCAAGTTGCTGTGCTGTGGTGATGTC	480
Db	421 AGCTGCTTTCCATTCAACAAACTCGATGTGCAAGTTGCTGTGCTGTGGTGATGTC	480
Qy	481 ATTTCACTGGTAGCTGCATTCCGATGACCTTCTGATCACATCAACCAACAGGACCAAC	540
Db	481 ATTTCACTGGTAGCTGCATTCCGATGACCTTCTGATCACATCAACCAACAGGACCAAC	540
Qy	541 AGATCAGCCTGTCTCGACCTCACCAAGTTGGATGAACACTCAATACTATTAAGTGGTACAAC	600
Db	541 AGATCAGCCTGTCTCGACCTCACCAAGTTGGATGAACACTCAATACTATTAAGTGGTACAAC	600
Qy	601 CTGATTGACTGCAAGTACTTCGCTCCCTGGTGTAGTGACACTTGCTATACC	660
Db	601 CTGATTGACTGCAAGTACTTCGCTCCCTGGTGTAGTGACACTTGCTATACC	660
Qy	661 ACGATTATCCACACTTGACCCATGGACTGCAAACACTGACAGCTGCCATTAGCAGAAAGCA	720
Db	661 ACGATTATCCACACTTGACCCATGGACTGCAAACACTGACAGCTGCCATTAGCAGAAAGCA	720
Qy	721 CGAAGGCTAACCAATTGCTACTCCTGCATTACGTATGTTTACCCCTCCATATC	780
Db	721 CGAAGGCTAACCAATTGCTACTCCTGCATTACGTATGTTTACCCCTCCATATC	780
Qy	781 TTGAGGGTCATTCAAGGATCGAATCTCAGCCTGCTTCAATCAGTTGTTCCATTGAGAATC	840
Db	781 TTGAGGGTCATTCAAGGATCGAATCTCAGCCTGCTTCAATCAGTTGTTCCATTGAGAATC	840
Qy	841 AGATCCATGAAGCTTACATCGTTCTAGACCATATGCTGCTCTGAACACCTTGGTAAC	900
Db	841 AGATCCATGAAGCTTACATCGTTCTAGACCATATGCTGCTCTGAACACCTTGGTAAC	900
Qy	901 CTGTTACTATATGTTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACAGTGAGA	960
Db	901 CTGTTACTATATGTTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACAGTGAGA	960
Qy	961 TGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCTTGA	1020
Db	961 TGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCTTGA	1020

No.	Score	Match	Length	DB	ID	Description
1	210	20.6	744	14	BM723768	BM723768 UI-E-EO1-
2	126.6	12.4	623	14	BQ038875	BQ038875 pgnlc.pk0
3	115.6	11.3	641	14	BQ396255	BQ396255 NISC_ng19
4	114.6	11.2	638	9	AL675845	AL675845 AL675845
5	109.4	10.7	877	12	BG402029	BG402029 602466748
6	108.8	10.7	663	13	BM426517	BM426517 pgf2n.pk0
c 7	107.4	10.5	1101	17	CNS0532S	AL318925 Tetraodon
8	106.2	10.4	491	12	BG712193	BG712193 pglin.pk0
9	103	10.1	609	9	AL588350	AL588350 AL588350
10	102	10.0	520	9	AI663305	AI663305 uk27c10.y
11	100.4	9.8	2542	11	AK017378	AK017378 Mus muscu
12	100.4	9.8	3001	11	AK005013	AK005013 Mus muscu
13	100	9.8	422	10	BB847918	BB847918 BB847918
14	99.6	9.8	801	13	BG924078	BG924078 602823635
15	98.4	9.6	606	17	AZ953874	AZ953874 2M0219L17
16	97.2	9.5	851	13	BI833118	BI833118 603090834
c 17	95.8	9.4	408	13	BI401676	BI401676 MI-P-CP0-

## RESULT 1

BM723768

LOCUS BM723768 744 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EO1-aix-g-16-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone  
UI-E-EO1-aix-g-16-0-UI 5', mRNA sequence.

ACCESSION BM723768

VERSION BM723768.1 GI:19045099

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 744)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source 1..744  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-EO1-aix-g-16-0-UI"  
/clone\_lib="UI-E-EO1"  
/tissue\_type="fetal eye"  
/dev\_stage="fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATAACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT      217 a    168 c    126 g    233 t  
ORIGIN

Query Match                20.6%; Score 210; DB 14; Length 744;  
Best Local Similarity    98.8%; Pred. No. 1.8e-51;  
Matches 243; Conservative 0; Mismatches 0; Indels 3; Gaps 3;  
  
 Qy    775 CATATCTGAGGGTCATTCAAGGATCGAATCTCAGCCTGCTTCATTCAATCAGTTGTTCCATTG 834  
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db    1 CATATCTGAGGGTCATT- GGATCGAATCTC-GCCTGCTTCATTCAATCAGTTGTTCCATTG 58  
  
 Qy    835 AGAACATCAGATCCATGAAGCTTACATCGTTCTAGACCATTATGCTGCTGAAACACCTTT 894  
       ||||||| ||||| ||||| ||||| |||||  
 Db    59 AGAACATCAGATCCATGAAGCTTACATCGTTCTAGACCATT-A-GCTGCTGAAACACCTTT 117  
  
 Qy    895 GTTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACA 954  
       ||||||| ||||| ||||| ||||| |||||  
 Db    118 GTTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTCAGCAGGCTGTGCTCAACA 177  
  
 Qy    955 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAAC 1014  
       ||||||| ||||| ||||| ||||| |||||  
 Db    178 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAAC 237  
  
 Qy    1015 CCTTGA 1020  
       |||||  
 Db    238 CCTTGA 243

#### AI663305

LOCUS                    AI663305                520 bp           mRNA          linear     EST 10-MAY-1999  
 DEFINITION              uk27c10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone  
                           IMAGE:1970226 5' similar to SW:P2YR\_RAT P49651 P2Y PURINOCEPTOR 1  
                           ;, mRNA sequence.  
 ACCESSION              AI663305  
 VERSION                AI663305.1            GI:4766888  
 KEYWORDS              EST.  
 SOURCE                house mouse.  
 ORGANISM              Mus musculus  
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE            1 (bases 1 to 520)  
 AUTHORS               Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
                      Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person  
                      ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
                      ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
                      Waterston,R. and Wilson,R.  
 TITLE                 The WashU-NCI Mouse EST Project 1999  
 JOURNAL              Unpublished (1999)  
 COMMENT              Other\_ESTs: uk27c10.x1  
                          Contact: Marra M/WashU-NCI Mouse EST Project 1999  
                          Washington University School of Medicine  
                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
                          Tel: 314 286 1800  
                          Fax: 314 286 1810  
                          Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

**MGI:986966**  
Seq primer: custom primer used  
High quality sequence stop: 490.  
**FEATURES** Location/Qualifiers  
source 1. .520  
/organism="Mus musculus"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1970226"  
/clone\_lib="Sugano mouse kidney mkia"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGCCCTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."  
**BASE COUNT** 127 a 126 c 107 g 160 t  
**ORIGIN**

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Query Match      10.0%; Score 102; DB 9; Length 520;
Best Local Similarity 53.4%; Pred. No. 3.3e-19;
Matches 238; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy   62 CTTTGAAATTGCACTGATGAAACATCCCCTCAAGATGCACTACCTCCCTGTTATT 121
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   73 CTTGTGAGAATTGGTGGCAACAGAGGCTATCTGAATAAGTACTACCTCTGCATT 132
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   122 ATGGCATTATCTTCCTCGTGGGATTCCAGGCAATGCAGTAGTGATATCCACTTACATT 181
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   133 ATGCAATCGAGTTCTTGGACTGCTGGGAATGTCAGTGTTGGCTACCTCT 192
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   182 TCAAAATGAGACCTTGGAAAGAGCAGCACCATTATGCTGAACCTGGCCTGCACAGATC 241
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   193 TCTGCATGAAGAACGGACAGCAGCAATGTCTATCTTTAACCTTCCATCTGACT 252
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   242 TGCTGTATCTGACCAGCCTCCCCCTCCCTGATTCACTACTATGCCAGTGGCGAAACTGGA 301
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   253 TTGCTTCTGTGCACCCCTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA 309
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   302 TCTTTGGAGATTCATGTGTAAGTTATCCGCTTCAGCTTCCATTCAACCTGTATAGCA 361
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   310 CCTATGGAGATGTTCTGTATAAGCAACCGATATGTGCTCACACCAACCTCTACACCA 369
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   362 GCATCCTTCCCTCACCTGTTCAAGCATCTCCGCTACTGTGTGATCATTACCCAATGA 421
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   370 GCATGCTTGTCACTGTCATTATCATGGACCGATATCTGCTCATGAAGTACCCGTCC 429
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   422 GCTGCTTCCATTCAACAAACTCGATGTGCAGTTGAGCCTGTGCTGTGGTGGATCA 481
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   430 GAGAACACTTCTACAAAAGAAGGAATTGCCATTAACTCGCTGGCTGTGGCCT 489
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   482 TTTCACTGGTAGCTGTCATTCCGATG 507
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   490 TAGTGACCTTAGAAGTTCTACCCATG 515
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1768	100.0	336	22	AAG80971	Human nGPCR54 #2.
2	1603.5	90.7	337	22	AAU04584	Human G-protein co
3	1602.5	90.6	337	22	AAU04375	Human G-protein co
4	1602.5	90.6	337	23	AAO15399	Human G protein-co
5	1602.5	90.6	337	23	ABB81902	Human G-protein co
6	1602.5	90.6	337	23	ABB83819	Human P2Y-like rec
7	1602.5	90.6	337	23	AAE21803	Human AXOR89 (G-pr
8	1602.5	90.6	337	23	ABB79438	Human P2Y1-li. Ho
9	1602.5	90.6	337	23	AAU77600	Human P2Y1-like G
10	1602.5	90.6	337	23	AAO14027	Human purinergic-r
11	1602.5	90.6	337	23	AAE16171	Human G-protein co
12	1275.5	72.1	276	23	ABB83818	Human P2Y-like rec
13	1098	62.1	230	22	AAM79297	Human protein SEQ
14	997	56.4	192	22	AAG80958	Human nGPCR54 #1.
15	881.5	49.9	179	22	ABB11082	Human P2Y purinoce
16	881.5	49.9	179	22	AAM80281	Human protein SEQ
17	525.5	29.7	373	22	AAE04389	Human P2-purinergi
18	525.5	29.7	373	23	AAU10983	Purinergic recepto
19	525.5	29.7	373	23	AAU10984	Purinergic re

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	525.5	29.7	373	2	JC4737	G protein-coupled
2	525	29.7	362	2	S33733	G protein-coupled
3	523.5	29.6	373	2	JC4162	P2Y receptor - bov
4	444.5	25.1	365	2	S68679	G protein-coupled
5	415	23.5	373	2	A47556	ATP receptor P2u -
6	414.5	23.4	420	2	I51667	thrombin receptor
7	390.5	22.1	375	2	A54946	P-2U nucleotide re
8	389.5	22.0	328	2	I55450	G protein-coupled
9	382	21.6	432	2	A43448	thrombin receptor
10	379	21.4	361	2	B45680	G protein-coupled
11	374.5	21.2	328	2	JC4800	P2Y6

## RESULT 1

JC4737

G protein-coupled receptor P2Y1 - human

N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence\_revision 16-Aug-1996 #text\_change 17-Nov-2000

C;Accession: JC4737; JC4615; S54253

R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M. Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A;Title: Cloning and tissue distribution of the human P2Y1 receptor.

A;Reference number: JC4737; MUID:96205320; PMID:8630005

A;Accession: JC4737

A;Molecule type: DNA

A;Residues: 1-373 &lt;JAN&gt;

A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439

R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P. Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A;Reference number: JC4615; MUID:96158962; PMID:8579591

A;Accession: JC4615

A;Molecule type: mRNA

A;Residues: 1-373 &lt;AYY&gt;

A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A;Experimental source: erythro leukemia cells  
 R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.  
 submitted to the EMBL Data Library, May 1995  
 A;Description: Cloning of a human putative P2Y receptor.  
 A;Reference number: S54253  
 A;Accession: S54253  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-137,139-373 <LEO>  
 A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836  
 C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds to both ADP and ATP, and has several serine/threonine phosphorylation residues in the carboxyl terminus.  
 C;Genetics:  
 A;Gene: p2Y1; GDB:P2RY1  
 A;Cross-references: GDB:677125; OMIM:601167  
 A;Map position: 3pter-3qter  
 C;Superfamily: ATP receptor P2u  
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F;52-77/Domain: transmembrane #status predicted <TM1>  
 F;88-111/Domain: transmembrane #status predicted <TM2>  
 F;124-152/Domain: transmembrane #status predicted <TM3>  
 F;171-191/Domain: transmembrane #status predicted <TM4>  
 F;214-237/Domain: transmembrane #status predicted <TM5>  
 F;261-282/Domain: transmembrane #status predicted <TM6>  
 F;305-328/Domain: transmembrane #status predicted <TM7>  
 F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
 F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent kinase) #status predicted

Query Match 29.7%; Score 525.5; DB 2; Length 373;  
 Best Local Similarity 34.5%; Pred. No. 1e-37;  
 Matches 106; Conservative 64; Mismatches 118; Indels 19; Gaps 3;  
  
 Qy 24 CTDENIPLKMHYLPVIIYGIIFLVGFPGNNAVISTYIFKMRPWKSSTIIMLNLA  
 Db 42 CALTKTGFQFYYPAVVILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV  
  
 Qy 84 TSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIHPMSCFS 143  
 Db 102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLGYGSILFLTCISAHRYSGVVYPLKSLG 161  
  
 Qy 144 IHKTRCAVVAACAVVIIISLVAVIPMTFLITSTNRNTNRS-ACLDLTSSDELNTIKWYNLIL 202  
 Db 162 RLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTTICYDTSDEYLRSYIFIYSMCT 221  
  
 Qy 203 TASTFCLPLVIVTLCYTTIHTLTHGLQTDCLKQKARRLTILLLA  
 Db 222 TVAMFCVPLVLILGYGLIVRALIYKLDNSPLRRKSIYLVIVLTVFAVSYIPFHVMKT 281  
  
 Qy 263 IQDRISACFQSVPPLRIRSMKLTSLDH-----YAALNTFGNLLLYVVVSDNFQQ 312  
 Db 282 MNLRARLDFQTPA-----MCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333  
  
 Qy 313 AVCSTVR 319  
 Db 334 RLSRATR 340

## RESULT 2

S33733

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-Sep-1999

C;Accession: S33733  
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.;  
Burnstock, G.; Barnard, E.A.  
FEBS Lett. 324, 219-225, 1993  
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.  
A;Reference number: S33733; MUID:93285340; PMID:8508924  
A;Accession: S33733  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-362 <WEB>  
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.7%; Score 525; DB 2; Length 362;  
Best Local Similarity 33.5%; Pred. No. 1.1e-37;  
Matches 113; Conservative 62; Mismatches 136; Indels 26; Gaps 5;

Qy 1 MNEPLDYLANASDFPDYAA---AFGN----CTDENIPLKMHYLPVIYGIIFLVGFPNAV 53  
| | | | | : | | | || | : : : || | : | | | : | | | : | | | : | | | : |  
Db 1 MTEALISAALNGTQPPELLAGGWAGGNATTKCSLTKTGFQFYLPVTYILVFITGFLGNSV 60

Qy 54 VISTYIFKMRPWKSSIIIMLNLAETDLYLTSPLPFLIHYYASGENWIFGDFMCKFIRFSF 113  
| : | | | | : : | | | | | : | | | | | : | | | | | | | | | | | | | | |  
Db 61 AIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFNKTDWIFGDVMCKLQRFIF 120

Qy 114 HFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLI- 172  
| | | | | | | : | | : | : | | : | | | | | | | | | | | | | | | | | | |  
Db 121 HVNLYGSILFLTCISVHRYTGVVHPLKSLGRKKNAVYVSSLVWALVVAIAPILFYSG 180

Qy 173 TSTNRNRSACLDLTSSDELNTIKWYNLILTASTFCPLPLVIVTLCYTTIHTLTHGLQTD 232  
| | | | | | | : | : | : | : | : | | | | | | | | | | | | | | | | | |  
Db 181 TGVRNNKTITCYDTTADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDN 240

Qy 233 SCLKQKARRLTILLLAFYVCFLPFHILRVIQDRISACFQSVPRLIRSMKLTFLDH-- 290  
| | : | : | | : | | : | | : | | | | | | | | | | | | | | | | | | | |  
Db 241 SPLRRKSIYLVIIIVLTVFAVSYLPFHVMKTLNLRARLDFQ-----TPQMCAPNDKVV 292

Qy 291 -----YAALNTFGNLLLYVVVSDNFQQAVCSTVR 319  
| : | : | : | : | | : | | : | |  
Db 293 ATYQVTRGLASLNCSVDPILYFLAGDTFRRRLSRATR 329

RESULT 3  
JC4162  
P2Y receptor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 12-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 24-Sep-1999  
C;Accession: JC4162  
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.  
Biochem. Biophys. Res. Commun. 212, 648-656, 1995  
A;Title: Cloning and characterisation of a bovine P2Y receptor.  
A;Reference number: JC4162; MUID:95352058; PMID:7626079  
A;Accession: JC4162  
A;Molecule type: mRNA  
A;Residues: 1-373 <HEN>  
A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485  
A;Experimental source: aortic endothelial cell  
C;Genetics:  
A;Gene: bovp2y  
C;Superfamily: ATP receptor P2u  
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
F;52-77/Domain: transmembrane #status predicted <TM1>  
F;88-111/Domain: transmembrane #status predicted <TM2>  
F;124-150/Domain: transmembrane #status predicted <TM3>  
F;171-191/Domain: transmembrane #status predicted <TM4>  
F;214-237/Domain: transmembrane #status predicted <TM5>  
F;261-282/Domain: transmembrane #status predicted <TM6>  
F;305-328/Domain: transmembrane #status predicted <TM7>

## RESULT 5

A47556

## ATP receptor P2u - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999

C;Accession: A47556

R; Lustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A; Reference number: A47556; MUID:93281707; PMID:7685114

A;Accession: A47556

A; Status: preliminary

A; Molecule type: mRNA

A;Residues: 1-373 <LU:

#### A: Cross-references: GB:

C:Superfamily: ATP receptor P2u

C:Keywords: transmembrane prote

• [View Details](#) • [Edit Details](#) • [Delete](#)

Query Match 23.5% - Score 415 - DB 2 - Length 373 -

**Best Local Similarity** 33.7%: Pred. No. 3 2e-28:

Matches 82, Conservative 30, Mismatches 101, Indexes 10, Gaps

28 NTPLKMHYLPVLYGTLIELVGFPGNAVVIYSTLEKMPWKSSTIIMLNLAQTDILYLTSLP 87

28 NEDEKYL I BYSYCVCYCLICLICLVINXIELGRKTWNASTTYMEHLAVSDSLXASLD 87

28 NEDFKRYVEEPVSTGVVCEIGECLINVVALYIFECRERKTIWNASTIIMFHLAVSDSLTIAASLP 87

88 FLTHYIASGENWIFGDFMCKFTRFSFHFNLYSSILFLTCFSITFRYCIVTHPMSCFSIHKI 147

88 LIVVVVYARCDHWHFESTVILCKLIVPFLFXTNLKGSILIELTCISVWRCIGVILRHLHSIWRGPA 147

CV 148 BCNVVAGAVWILISVYAVLPMTELITCTNRTNRSAGLDLTCSDELNTIKYDULTAGSTE 307

QY 148 RCAA VACAVVVIISLVA VIFPMI FLLTIS KINKRSAC LDEI SSDEL NTIRW YINL LIASTF 207

DB 148 RYARRVAAVVWVLACQAPVLYFVTTSVRGTRITCHDTARELFSHFVAYSSVMLGLLF 207

SY 308 GLPLVLTGKTTILVTL-- TUGLDTBSCIKOKABRITULLAEXYGEI DEWIL 360

202. НУРСЕКИЙ САНКИ МАРДИЛ КЕРМЕССЕГІЛДЕ НУРСЕКИТИНІҢ НЫНА СЕЛДЕНІКІТ 211

208 AVPFPSVILVLCYVLMARRKLEKPAYGTTGGLPR---AKRKSVRTIALVLAVFALCFLPFRVT 264

Qy      261 RVI 263  
| :  
Db      265 RTL 267